

Table S2: Genes regulated by RyhB in both CFT073 and MG1655¹

Operons regulated by RyhB in both CFT073 and MG1655, which encode at least one protein with iron as cofactor

Functions ²	Operon ²	Gene ²	Protein product ²	c-number ²	RNA-seq fold change ³		
					fur ⁻ /wt	ryhB ⁻ /wt	fur ⁺ ryhB ⁻ /wt
Respiration and Metabolism							
	<i>dmsABC</i>	<i>dmsA</i>	dimethyl sulfoxide reductase, anaerobic, subunit A	c1031	0.15	1.00	1.00
		<i>dmsB</i>	dimethyl sulfoxide reductase, anaerobic, subunit B	c1032	0.22	0.93	1.00
		<i>dmsC</i>	dimethyl sulfoxide reductase, anaerobic, subunit C	c1033	0.38	1.00	1.00
	<i>hybOABCDEFG</i>	<i>hybO</i>	hydrogenase 2, small subunit	c3734	0.38	1.07	0.93
		<i>hybA</i>	hydrogenase 2 4Fe-4S ferredoxin-type component	c3733	0.29	1.07	0.93
		<i>hybB</i>	predicted hydrogenase 2 cytochrome b type component	c3732	0.27	1.07	0.87
		<i>hybC</i>	hydrogenase 2, large subunit	c3731	0.41	1.07	0.87
		<i>hybD</i>	predicted maturation element for hydrogenase 2	c3730	0.41	1.00	0.81
		<i>hybE</i>	hydrogenase 2-specific chaperone	c3729	0.41	1.00	0.87
		<i>hybF</i>	protein involved with the maturation of hydrogenases 1 and 2	c3728	0.47	1.00	0.81
		<i>hybG</i>	hydrogenase 2 accessory protein	c3727	0.54	0.87	0.81
	<i>hycABCDEFGHI</i>	<i>hycA</i>	regulator of the transcriptional regulator FhlA	c3285	0.57	1.07	0.87
		<i>hycB</i>	hydrogenase 3, Fe-S subunit	c3284	0.57	1.07	0.76
		<i>hycC</i>	hydrogenase 3, membrane subunit	c3283	0.57	1.07	0.81
		<i>hycD</i>	hydrogenase 3, membrane subunit	c3282	0.66	1.07	0.87
		<i>hycE</i>	hydrogenase 3, large subunit	c3281	0.54	1.07	0.81
		<i>hycF</i>	formate hydrogenlyase complex iron-sulfur protein	c3280	0.54	1.07	0.87
		<i>hycG</i>	hydrogenase 3 and formate hydrogenase complex, HycG subunit	c3279	0.57	1.07	0.87
		<i>hycH</i>	protein required for maturation of hydrogenase 3	c3278	0.50	1.00	0.81
		<i>hycl</i>	protease involved in processing C-terminal end of HycE	c3277	0.57	1.00	0.81
	<i>hypABCDE-fhlA</i>	<i>hypA</i>	protein involved in nickel insertion into hydrogenases 3	c3286	0.57	1.00	0.76
		<i>hypB</i>	GTP hydrolase involved in nickel liganding into hydrogenases	c3287	0.41	1.07	1.07
		<i>hypC</i>	protein required for maturation of hydrogenases 1 and 3	c3288	0.44	1.00	1.00
		<i>hypD</i>	protein required for maturation of hydrogenases	c3289	0.44	1.00	0.93
		<i>hypE</i>	carbamoyl phosphate phosphatase, hydrogenase 3 maturation protein	c3290	0.57	1.00	0.93
		<i>fhlA</i>	DNA-binding transcriptional activator	c3291	0.71	1.00	0.87
	<i>frdABCD</i>	<i>frdA</i>	fumarate reductase (anaerobic) catalytic and NAD/flavoprotein subunit	c5242	0.57	1.07	1.41
		<i>frdB</i>	fumarate reductase (anaerobic), Fe-S subunit	c5241	0.54	1.07	1.41
		<i>frdC</i>	fumarate reductase (anaerobic), membrane anchor subunit	c5240	0.54	1.07	1.32
		<i>frdD</i>	fumarate reductase (anaerobic), membrane anchor subunit	c5239	0.50	1.00	1.32
	<i>narGHJI</i>	<i>narG</i>	nitrate reductase 1, alpha subunit	c1685	0.47	0.93	1.00
		<i>narH</i>	nitrate reductase 1, beta (Fe-S) subunit	c1686	0.54	0.93	1.00
		<i>narJ</i>	molybdenum-cofactor-assembly chaperone subunit (delta subunit) of nitr	c1687	0.57	0.93	0.93
		<i>narI</i>	nitrate reductase 1, gamma (cytochrome b(NR)) subunit	c1688	0.71	1.00	1.00
	<i>nrfABCDEFG</i>	<i>nrfA</i>	nitrite reductase, formate-dependent, cytochrome	c5066	0.13	1.00	1.41
		<i>nrfB</i>	nitrite reductase, formate-dependent, penta-heme cytochrome c	c5067	0.09	0.93	1.32
		<i>nrfC</i>	formate-dependent nitrite reductase, 4Fe4S subunit	c5068	0.11	0.93	1.23
		<i>nrfD</i>	formate-dependent nitrite reductase, membrane subunit	c5069	0.09	1.00	1.32
		<i>nrfE</i>	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfE	c5070	0.18	1.00	1.07
		<i>nrfF</i>	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfF	c5071	0.33	0.93	0.87
		<i>nrfG</i>	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfG	c5072	0.44	1.00	1.00
	<i>ynfEFGH-dmsD</i>	<i>ynfE</i>	oxidoreductase subunit	c1977	0.50	1.00	1.07
		<i>ynfF</i>	oxidoreductase subunit	c1978	0.14	1.07	0.87
		<i>ynfG</i>	oxidoreductase, Fe-S subunit	c1979	0.18	1.07	1.00
		<i>ynfH</i>	oxidoreductase, membrane subunit	c1981	0.19	1.00	0.93
		<i>dmsD</i>	twin-arginine leader-binding protein for DmsA and TorA	c1982	0.54	1.00	1.00
	<i>sdhCDAB</i>	<i>sdhC</i>	succinate dehydrogenase, membrane subunit, binds cytochrome b556	c0798	0.57	1.00	0.66

	<i>sdhD</i>	succinate dehydrogenase, membrane subunit, binds cytochrome b556	c0800	0.62	1.00	1.07
	<i>sdhA</i>	succinate dehydrogenase, flavoprotein subunit	c0801	0.54	1.00	0.93
	<i>sdhB</i>	succinate dehydrogenase, FeS subunit	c0802	0.54	1.00	0.93
<i>nuoABCDEGHJKLMN</i>	<i>nuoA</i>	NADH:ubiquinone oxidoreductase, membrane subunit A	c2829	0.54	0.93	0.93
	<i>nuoB</i>	NADH:ubiquinone oxidoreductase, chain B	c2828	0.47	1.00	1.00
	<i>nuoC</i>	NADH:ubiquinone oxidoreductase, chain C,D	c2827	0.38	1.00	1.00
	<i>nuoE</i>	NADH:ubiquinone oxidoreductase, chain E	c2826	0.47	1.00	1.07
	<i>nuoF</i>	NADH:ubiquinone oxidoreductase, chain F	c2825	0.44	1.00	1.00
	<i>nuoG</i>	NADH:ubiquinone oxidoreductase, chain G	c2824	0.38	1.00	1.00
	<i>nuoH</i>	NADH:ubiquinone oxidoreductase, membrane subunit H	c2823	0.35	1.00	1.00
	<i>nuoI</i>	NADH:ubiquinone oxidoreductase, chain I	c2822	0.38	1.00	1.00
	<i>nuoJ</i>	NADH:ubiquinone oxidoreductase, membrane subunit J	c2821	0.41	1.00	1.07
	<i>nuoK</i>	NADH:ubiquinone oxidoreductase, membrane subunit K	c2820	0.50	1.15	1.07
	<i>nuoL</i>	NADH:ubiquinone oxidoreductase, membrane subunit L	c2819	0.41	1.00	1.00
	<i>nuoM</i>	NADH:ubiquinone oxidoreductase, membrane subunit M	c2818	0.47	1.07	0.93
	<i>nuoN</i>	NADH:ubiquinone oxidoreductase, membrane subunit N	c2817	0.47	1.00	0.93
<i>ydiJIH</i>	<i>ydiJ</i>	predicted FAD-linked oxidoreductase	c2082	0.35	1.00	0.93
	<i>ydiI</i>	esterase	c2081	0.54	1.00	0.93
	<i>ydiH</i>	predicted protein	c2080	1.87	1.00	0.87
<i>fumA</i>	<i>fumA</i>	fumarate hydratase (fumarase A), aerobic Class I	c2004	0.41	1.00	0.81
<i>pflA</i>	<i>pflA</i>	pyruvate formate lyase activating enzyme 1	c1038	0.62	1.00	1.23
Unknown	<i>yjiML</i>	predicted 2-hydroxyglutaryl-CoA dehydratase	c5418	0.44	1.00	1.07
	<i>yjiL</i>	predicted ATPase, activator of (R)-hydroxyglutaryl-CoA dehydratase	c5417	0.38	1.00	0.93
Fe-S assembly						
<i>iscSUA-hscBA-fdx-iscX</i>	<i>iscS</i>	cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent	c3056	0.57	1.07	1.15
	<i>iscU</i>	FeS cluster assembly scaffold	c3055	0.76	1.07	1.07
	<i>iscA</i>	FeS cluster assembly protein	c3053	0.76	1.00	1.07
	<i>hscB</i>	DnaJ-homologue co-chaperone protein Hsc20	c3052	0.71	1.00	1.07
	<i>hscA</i>	DnaK-like molecular chaperone specific for IscU	c3051	0.66	1.00	1.23
	<i>fdx</i>	[2Fe-2S] ferredoxin	c3050	0.57	1.00	1.23
	<i>iscX</i>	conserved protein	c3049	0.62	1.07	1.15
<i>mrp</i>	<i>mrp</i>	P-loop NTPase family protein mrp	c2641	0.54	1.00	0.87
Oxidative stress						
	<i>sodB</i>	superoxide dismutase, Fe	c2050	0.09	1.07	1.23

Genes regulated by RyhB in both CFT073 and MG1655 but lack iron as cofactor

Transport						
<i>oppABCDF</i>	<i>oppA</i>	periplasmic-binding component of an ABC superfamily oligopeptide trans	c1707	0.50	1.15	0.87
	<i>oppB</i>	oligopeptide transporter subunit; membrane component of ABC superfamily	c1708	0.41	1.15	0.76
	<i>oppC</i>	membrane component of an ABC superfamily oligopeptide transporter	c1709	0.38	1.07	0.81
	<i>oppD</i>	oligopeptide transporter subunit; ATP-binding component of ABC superfamily	c1710	0.44	1.15	0.76
	<i>oppF</i>	ATP-binding subunit of oligopeptide ABC transporter	c1711	0.41	1.07	0.76
<i>dppBCDF</i>	<i>dppB</i>	dipeptide transporter; membrane component of ABC superfamily	c4358	0.22	1.07	1.23
	<i>dppC</i>	dipeptide transporter; membrane component of ABC superfamily	c4357	0.20	1.15	1.23
	<i>dppD</i>	dipeptide transporter; ATP-binding component of ABC superfamily	c4356	0.27	1.15	1.23
	<i>dppF</i>	dipeptide transporter; ATP-binding component of ABC superfamily	c4355	0.25	1.15	1.15
<i>ydeA</i>	<i>sotB</i>	predicted arabinose transporter	c1950	2.14	1.07	1.07
<i>ynfM</i>	<i>ynfM</i>	predicted transporter	c1987	2.83	0.93	0.71
<i>yohJK</i>	<i>yohJ</i>	conserved inner membrane protein	c2673	2.00	0.93	1.23
	<i>yohK</i>	predicted inner membrane protein	c2674	0.87	0.93	1.00
<i>shiA</i>	<i>shiA</i>	shikimate transporter	c2443	3.48	1.00	0.76
Metabolism						
<i>arnBCADTEF</i>	<i>arnB</i>	UDP-4-amino-4-deoxy-L-arabinose alpha-ketoglutarate aminotransferase	c2795	0.31	0.93	0.93

<i>arnC</i>	Undecaprenyl-phosphate 4-amino-4-deoxy-L-arabinose transferase	c2796	0.35	0.93	0.76
<i>arnA</i>	bifunctional UDP-L-Ara4N formyltransferase/UDP-GlcA C-4'-decarboxylas	c2797	0.31	0.93	0.76
<i>yfbH</i>	conserved protein	c2798	0.31	0.93	0.76
<i>arnT</i>	4-amino-4-deoxy-L-arabinose transferase	c2799	0.27	0.93	0.71
<i>arnE</i>	hypothetical protein	c2800	0.29	0.93	0.66
<i>arnF</i>	Hypothetical protein yfbJ	c2801	0.35	0.93	0.76
<i>ilvBN</i>	<i>ilvB</i> acetolactate synthase I, large subunit	c4596	0.44	1.07	1.07
	<i>ilvN</i> acetolactate synthase I, small subunit	c4595	0.54	1.07	1.07
<i>bioA</i>	<i>bioA</i> adenosylmethionine-8-amino-7-oxononanoate aminotransferase	c0853	2.30	1.07	1.15
Unknown Transport					
<i>psiE</i>	<i>psiE</i> predicted phosphate starvation inducible protein	c5001	4.00	1.07	1.00
<i>yjfY</i>	<i>yjfY</i> predicted protein	c5289	2.14	1.00	1.00

¹ CFT073 operons that have at least one gene regulated by RyhB in both CFT073 and MG1655 grown in glucose minimal media anaerobically.

² Gene functions, predicted operons, gene names, protein annotations and c numbers were obtained from EcoCyc.

³ Fold change in RNA-seq expression of CFT073 *Δfur* (WAM5491), *ΔryhB* (WAM5497) or *Δfur ΔryhB* (WAM5499) compared to wild type (WAM4505).

Those genes which showed > 2-fold change (upregulation or down-regulation) in RNA-seq with p-value<0.05 in *Δfur* but returned to wild type level in *Δfur ΔryhB* are indicated in bold.